1/66

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Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu 50 55 60

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· Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

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Thr	Ala	Ala 275		Gly	Tyr	Ala	Gly 280		Arg	Val	Ala	Val 285	Thr	Phe	Phe
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Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala 85 90 95

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Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met 165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Met 180 185 190

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Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu

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60

120 -

PCT/EP2003/014679 WO 2004/057333

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660

720

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Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

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175 170 165 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 230 <210> 11 2457 . <211> <212> DNA artificial sequence <213> <220> alpha2a adrenergic receptor-cam cDNA sequence <223> <400> 11 atgggctacc catacgacgt cccagactac gccagcatgg gctcactgca gccggatgcc 60 ggcaacagca gctggaacgg gaccgaagcg cccggaggcg gcacccgagc cacccttac 120 180 tecetgeagg tgacactgae getggtttge etggetggee tgeteatget gtteacagta 240 tttggcaacg tgctggttat tatcgcggtg ttcaccagtc gcgcgctcaa agctccccaa 300 aacctcttcc tggtgtccct ggcctcagcg gacatcctgg tggccacgct ggtcattccc ttttctttgg ccaacgaggt tatgggttac tggtactttg gtaaggtgtg gtgtgagatc 360 tatttggctc tcgacgtgct cttttgcacg tcgtccatag tgcacctgtg cgccatcagc 420 cttgaccgct actggtccat cacgcaggcc atcgagtaca acctgaagcg cacgccgcgt 480 cgcatcaagg ccatcattgt caccgtgtgg gtcatctcgg ctgtcatctc cttcccgcca 540 ctcatctcca tagagaagaa gggcgctggc ggcgggcagc agccggccga gccaagctgc 600 aagatcaacg accagaagtg gtatgtcatc tectegteea teggtteett ettegegeet 660 tgcctcatca tgatcctggt ctacgtgcgt atttaccaga tcgccaagcg tcgcacccgc 720 780 gtgcctccca gccgccgggg tccggacgcc atggtgagca agggcgagga gctgttcacc 840 ggggtggtgc ccatcctggt cgagctggac ggcgacgtaa acggccacaa gttcagcgtg teeggegagg gegagggega tgecacetae ggeaagetga eeetgaagtt catetgeace 900

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Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr 85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
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Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe 115 120 . 125

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Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile 165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly 180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr 195 200 205

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Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu 85 90 95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

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Ph€	e Gl	у Туз	r Gly	7 Let 805		ı Cys	B Phe	Ala	a Arç 810		r Pro	Ası) His	Met 815	: Lys

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Val	Lys 850	Phe	Glu	Gly	Asp	Thr 855	Leu	Val	Asn	Arg	Ile 860	Glu	Leu	Lys	Gly	
Ile 865	Asp	Phe	Lys	Glu	Asp 870	Gly	Asn	Ile	Leu	Gly 875	His	Lys	Leu	Glu	Tyr 880	
Asn	Tyr	Asn	Ser	His 885	Asn	Val	Tyr	Ile	Met 890	Ala	Asp	Lys	Gln	Lys 895	Asn	
Gly	Ile	Lys	Val 900	Asn ·	Phe	Lys	Ile	Arg 905	His	Asn	Ile	Glu	Asp 910	Gly	Ser	
Val	Gln	Leu 915	Ala	Asp	His	Tyr	Gln 920	Gln	Asn	Thr	Pro	Ile 925	Gly	Asp	Gly	
Pro	Val 930	Leu	Leu	Pro	Asp	Asn 935	His	Tyr	Leu	Ser	Tyr 940	Gln	Ser	Ala	Leu	
Ser 945	Lys	Asp	Pro	Asn	Glu 950	Lys	Arg	Asp	His	Met 955		Leu	Leu	Glu	Phe 960	
Val	Thr	Ala	Ala	Gly 965	Ile	Thr	Leu	Gly	Met 970	Asp	Glu	Leu	Tyr	Lys 975		
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acc	aact	act	ttgt	ggtg	tc a	ctgg	cggc	g gc	cgac	atcg	cag	ıtggg	ıtgt	gcto	gccatc	180
000	+++~		+020	cato	200		· ·~~++	· a + a	cact	coct		ים רתר	rcta	cctc	ttcatt	240

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gaccgctaca	ttgccatccg	catcccgctc	cggtacaatg	gcttggtgac	cggcacgagg	360
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Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala 65 70 75 80	
Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala 85 90 95	
Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn 100 105 110	
Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp 115 120 125	

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn . 130 $$135\$

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Val	Tyr	Phe	Asn 180	Phe	Phe	Ala	Cys	Val 185	Leu	Val	Pro	Leu	Leu 190	Leu	Met
Leu	Gly	Val 195	Tyr	Leu	Arg	Ile	Phe 200	Leu	Ala	Ala	Arg	Arg 205	Gln	Leu	Lys
Gln	Met 210	Glu	Val	Ser	Lys	Gly 215	Glu	Glu	Leu	Phe	Thr 220	Gly	Val	Val	Pro
Ile 225	Leu	Val	Glu	Leu	Asp 230	Gly	Asp	Val	Asn	Gly 235	His	Lys	Phe	Ser	Val 240
Ser	Gly	Glu	Gly	Glu 245	Gly	Asp	Ala	Thr	Tyr 250	Gly	Lys	Leu	Thr	Leu 255	Lys
Phe	Ile	Cys	Thr 260	Thr	Gly	Lys	Leu	Pro 265	Val	Pro	Trp	Pro	Thr 270	Leu	Val
Thr	Thr	Leu 275	Thr	Trp	Gly	Val	Gln 280	Cys	Phe	Ser	Arg	Tyŕ 285		Asp	His
Met	Lys 290	Gln	His	Asp	Phe	Phe 295		Ser	Ala	Met	Pro 300		Gly	Tyr	Val
Gln 305	Glu	Arg	Thr	Ile	Phe 310		Lys	Asp	Asp	Gly 315		Tyr	. Lys	Thr	Arg 320
Ala	Glu	Val	Lys	Phe 325	Glu	Gly	Asp	Thr	330		Asn	Arg	, Ile	Glu 335	
Lys	Gly	Ile	Asp 340		Lys	Glu	Asp	Gly 345		ılle	. Leu	ı Gly	, His 350		: Lev
Glu	Tyr	Asn 355		Ile	s Ser	His	360		. Туг	: Ile	. Thr	365		. Lys	s Glr
Lys	Asn		, Ile	Lys	: Ala	Asr		e Lys	s Ile	e Arg	y His		n Ile	e Glu	ı Ası

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Asp	Gly	Pro	Val	Leu 405	Leu	Pro	Asp	Asn	His 410	Tyr	Leu	Ser	Thr	Gln 415	Ser
Ala	Leu	Ser	Lys 420	Asp	Pro	Asn	Glu	Lys 425	Arg	Asp	His	Met	Val 430	Leu	Leu
Glu	Phe	Val 435	Thr	Ala	Ala	Gly	Ile 440	Thr	Leu	Gly	Met	Asp 445	Glu	Leu	Tyr
Lys	Leu 450	Gln	Lys	Glu	Val	His 455	Ala	Ala	Lys	Ser	Leu 460	Ala	Ile	Ile	Val
Gly 465	Leu	Phe	Ala	Leu	Cys 470	Trp	Leu	Pro	Leu	His 475	Ile	Ile	Asn	Cys	Phe 480
Thr	Phe	Phe	Cys	Pro 485	Asp	Суз	Ser	His	Ala 490	Pro	Leu	Trp	Leu	Met 495	Tyr
Leu	Ala	Ile	Val 500	Leu	Ser	His	Thr	Asn 505	Ser	∀al	Val	Asn	Pro 510	Phe	Ile
Tyr	Ala	Tyr 515	Arg	Ile	Arg	Glu	Phe 520	Arg	Gln	Thr	Phe	Arg 525	Lys	Ile	Ile
Arg	Ser 530	His	Val	Leu	Arg	Gln 535	Gln	Glu	Pro	Phe	Lys 540	Ala	Ala	Gly	Thr
Ser 545	Ala	Arg	Val	Met	Val 550	Ser	Lys	Gly	Glu	Glu 555		Phe	Thr	Gly	Val 560
Val	Pro	Ile	Leu	Val 565		Leu	Asp	Gly	Asp 570		Asn	Gly	His	Lys 575	Phe
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Leu	Lys	Phe 595		Cys	Thr	Thr	Gly 600		Leu	Pro	Val	Pro 605		Pro	Thr
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Thr	Arg	Ala	Glu 660	Val	Lys	Phe	Glu	Gly 665	Asp	Thr	Leu	Val	Asn 670	Arg	Ile	
Glu	Leu	Lys 675	Gly	Ile	Asp	Phe	Lys 680	Glu	Asp	Gly	Asn	Ile 685	Leu	Gly	His	
Lys	Leu 690	Glu	Tyr	Asn	Tyr	Asn 695	Ser	His	Asn	Val	Tyr 700	Ile	Met	Ala	Asp	
Lys 705	Gln	Lys	Asn	Gly	Ile 710	Lys	Val	Asn	Phe	Lys 715	Ile	Arg	His	Asn	Ile 720	
Glu	Asp	Gly	Ser	Val 725	Gln	Leu	Ala	Asp	His 730	Tyr	Gln	Gln	Asn	Thr 735	Pro	
Ile	Gly	Asp	Gly 740	Pro	Val	Leu	Leu	Pro 745	Asp	Asn	His	Tyr	Leu 750	Ser	Tyr	
Gln	Ser	Ala 755	Leu	Ser	Lys	Asp	Pro 760		Glu	Lys	Arg	Asp 765	His	Met	.Val	
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cccggggccg	cggggccggg	ggcttcgggg	tccgggcacg	gagaggagcg	cggcgggggc	420
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<213> Mouse

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Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly Pro Thr Gly Ala
35 40 45

Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala Pro Gly Glu Pro 50 55 60

Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp Leu Glu Glu Ser 65 70 75 80

Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro Arg Arg Pro Asp 85 90 95

Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser Gln Val Lys Pro 100 105 110

Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala Gly Pro Gly Ala 115 120 125

Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly Ala Lys Ala Ser 130 135 140

Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe Thr Phe Val 145 150 155

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33/66	
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gcccaagagt cccaggggaa cacgggcctc ccagacgtgg agctccttag ccatgagctc	300
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Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro 50 55 60	
Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly Ser 65 70 75 80	
Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu Leu 85 90 95	
Ser His Glu Leu Lys Gly 100	
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Tyr _. A	rg Lys					٠									
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cgaaaq															
gtgaco															
actgc														_	
ctgga															
aacgg	ctcct	gctca	aggco	st go	gacga	aggaç	g gcc	etcto	ggc	ctga	ıgcgg	jcc a	accto	geeetg	
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Gly P	ro Met 35	Val	Ser	His	Thr	Ser 40	Val	Thr	Asn	Val	Gly 45	Pro	Arg	Val	
Gly L		' Leu	Pro	Leu	Ser 55	Pro	Arg	Leu	Leu	Pro 60	Thr	Ala	Thr	Thr	
Asn G	ly His	Pro	Gln	Leu 70	Pro	Gly	His	Ala	Lys 75	Pro	Gly	Thr	Pro	Ala 80	

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Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp 90 85 Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser 105 100 Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val 120 125 Met <210> 29 <211> 264 <212> PRT <213> artificial sequence <220> <223> PTHR-cam7 amino acid sequence <400> 29 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 5 Leu Asp Phe Lys Arg Lys Ala Arg Ser Met Val Ser Lys Gly Glu Glu 20 Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr 50 Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 85 Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser 105 100

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp

120

115

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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 245 250 . 255

Leu Gly Met Asp Glu Leu Tyr Lys 260

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Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Met 20 25 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 35 40 45

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
50 55 60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 65 70 75 80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 85 90 95

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln 100 105 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 115 120 125

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 130 135 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 145 150 155 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn . 165 170 175

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
· 180 185 190

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 195 200 205

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 210 215 220

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser 225 230 235 240

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 245 250 255

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 260 · 265 270

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<223> PTHR-cam8 amino acid sequence

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Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 35 40 45

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 50 55 60

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 65 70 75 80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 85 90 95

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met 100 105 110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 115 120 125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 130 135 140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 145 150 155 160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu 165 170 175

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 180 185 190

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 195. 200 205

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Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 210 215 220

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala 225 230 235 240

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 245 250 255

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 260 265 270

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Gly Pro Met Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 35 40 45

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 50 55 60

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 65 70 75 80

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 85 90 95

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro 100 105 110

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 115 120 125

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

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135 140 130 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 150 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 170 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 185 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr 235 230 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 245 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu 270 265 260 Leu Tyr Lys 275 <210> 33 <211> 289 <212> PRT <213> artificial sequence <220> <223> PTHR-cam5 amino acid sequence <400> 33 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 25 20 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val

40

35

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Gly Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 70 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 90 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His 115 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 130 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 155 145 150 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 170 165 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 185 180 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 195 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp 210 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 225 230 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser 245 250 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 260 265 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr

42/66

275 280 285

Lys

<210> 34
<211> 325
<212> PRT
<213> artificial sequence
<220>
<223> PTHR-caml amino acid sequence
<400> 34
Glu Val Gln Ala Glu Ile Lys Lys Ser

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala 65 70 75 80

Leu Glu Thr Leu Glu Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr 85 90 95

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
100 105 110

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys 115 120 125

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp 130 135 140

Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg 145 150 155 160

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro 165 170 · 175

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Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu . 215 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met 230 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His 250 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn 270 260 265 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu 280 285 275 Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His 290 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met 320 Asp Glu Leu Tyr Lys 325 <210> 35 <211> 339 <212> PRT <213> artificial sequence <223> PTHR-cam4 amino acid sequence Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 5

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr

44/66

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 150 155 Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro 170 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 180 185 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 200 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 235 240 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 245 250 255 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 260 265 270

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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 280

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr 295 300

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 305 310

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu

Leu Tyr Lys

<210> 36 <211> 354

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam3 amino acid sequence

<400> 36

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 5 10

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 20 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val 35

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr 50

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala 65 70 75

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp 85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser 105

					•		•								
Gly	Pro	Glu 115	Met	Val	Ser	ГÀЗ	Gly 120	Glu	Glu	Leu	Phe	Thr 125	Gly	Val	Val
Pro	Ile 130	Leu	Val	Glu	Leu	Asp 135	Gly	Asp	Val	Asn	Gly 140	His	Lys	Phe	Ser
Val 145	Ser	Gly	Glu	Gly	Glu 150	Gly	Asp	Ala	Thr	Tyr 155	Gly	Lys ·	Leu	Thr	Leu 160
Lys	Phe	Ile	Суз	Thr 165	Thr	Gly	Lys	Leu	Pro 170	Val	Pro	Trp	Pro	Thr 175	Leu
Val	Thr	Thr	Phe 180	Gly	Туг	Gly	Leu	Gln 185	Суз	Phe	Ala	Arg	Tyr 190	Pro	Asp
His	Met	Lys 195	Gln	His	Asp	Phe	Phe 200	Lys	Ser	Ala	Met	Pro 205	Glu	Gly	Tyr
Val	Gln 210	Glu	Arg	Thr	Ile	Phe 215	Phe	Lys	Asp	Asp	Gly 220	Asn	Tyr	Lys	Thr
Arg 225	Ala	Glu	Val	Гуз	Phe 230	Glu	Gly	Asp	Thr	Leu 235	Val	Asn	Arg	Ile	Glu 240
Leu	Lys	Gly	Ile	Asp 245		Lys	Glu	Asp	Gly 250		Ile	Leu	Gly	His 255	Lys
Leu	Glu	Tyr	Asn 260		Asn	Ser	His	Asn 265		Tyr	Ile	Met	Ala 270	Asp	Lys
Gln	Lys	Asn 275		Ile	Lys	Val	Asn 280		Lys	Ile	Arg	His 285	Asn	Ile	Glu
Asp	Gly 290		Val	Gln	Leu	Ala 295		His	Tyr	Gln	Gln 300		Thr	Pro	Ile
Gly 305		Gly	Pro	Val	Leu 310		Pro	Asp	Asn	His 315		Leu	. Ser	Туг	Gln 320
Ser	: Ala	. Lev	ı Ser	Lys 325	-	Pro	Asn	Glu	Lys 330		Asp	His	. Met	Val 335	Leu
Lev	ı Glu	ı Phe	• Val		: Ala	a Ala	a Gly	7 Ile 345	-	: Lev	ı Gly	Met	: Asp 350		Leu

47/66

Tyr Lys

<210> 37 <211> 368 <212> PRT <213> artificial sequence <220> <223> PTHR-cam10 amino acid sequence <400> 37 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr 25 20 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr 50 Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala 65 Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp 95 Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser 100 Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val 120 115 Met Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 135 . Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 155 150 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe.

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Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 180 185 190

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met 195 200 205

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 210 215 220

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 225 230 235 240

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 245 250 255

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu 260 265 270

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 275 280 285

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 290 295 300

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 305 310 315 320

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala 325 330 335

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu 340 345 350

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 355 360 365

<210> 38

<211> 518

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-PTHR-FRETcontrol amino acid sequence

<400> 38

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Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Met Val Ser Lys Gly Glu Leu 20 25 30

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn 35 40 45

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr 50 55 60

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 65 70 75 80

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 85 90 . 95

Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala 100 105 110

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 115 120 125

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 130 135 140

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 145 . 150 . 155 . 160

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 165 170 175

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 180 185 190

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 195 200 · 205

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 210 215 220

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 225 230 235 240

Asp	His	Met		Leu 245	Leu (Glu :	Phe		Thr 250	Ala	Ala	Gly	Ile	Thr 255	Leu
Gly	Met	Asp	Glu 260	Leu	Tyr :	Lys		Gly 265	Ser	Ser	Ser	Tyr	Ser 270	Tyr	Gly
Pro	Met	Val 275	Ser	His	Thr		Met 280	Val	Ser	Lys	Gly	Glu 285	Glu	Leu	Phe
Thr	Gly 290	Val	Val	Pro	Ile	Leu 295	Val	Glu	Leu	Asp	Gly 300	Asp	Val	Asn	Gly
His 305	Lys	Phe	Ser	Val	Ser 310	Gly	Glu	Gly	Glu	Gly 315	Asp	Ala	Thr	Tyr	Gly 320
Lys	Leu	Thr	Leu	Lys 325	Phe	Ile	Cys	Thr	Thr 330	Gly	Lys	Leu	Pro	Val 335	Pro
Trp	Pro	Thr	Leu 340	Val	Thr	Thr	Leu	Thr 345	Trp	Gly	Val	Gln	Cys 350	Phe	Ser
Arg	Tyr	Pro 355		His	Met	Lys	Gln 360	His	Asp	Phe	Phe	Lys 365	Ser	Ala	Met
Pro	Glu 370	_	Tyr	Val	Gln	Glu 375	Arg	Thr	Ile	Phe	Phe 380	Lys	Asp	Asp	Gly
Asn 385		Lys	Thr	Arg	Ala 390	Glu	Val	Lys	Phe	Glu 395		Asp	Thr	Leu	Val 400
Asn		r Ile	e Glu	Leu 405		Gly	Ile	Asp	Phe 410		Glu	Asp	Gly	/ Asn 415	ille
Leu	ı Gly	, His	Lys 420		Glu	Tyr	Asn	Tyr 425		e Ser	His	Asn	val 430		: Ile
Thr	Ala	ASP 435		Gln	Lys	Asn	Gly 440		e Lys	s Ala	a Asr	1 Phe 445		s Ile	e Arg
His	3 Asr 450		e Glı	ı Asp	Gly	Ser 455		. Glr	ı Leı	ı Ala	a Asp 460		з Ту	r Gli	n Gln
As:		r Pr	o Ile	e Gly	Asp 470		Pro	o Vai	l Le	u Le:		o Ası	p As:	n Hi	s Tyr 480

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Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp 485 490 495

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly 500 505 510

Met Asp Glu Leu Tyr Lys 515

<210> 39

<211> 1737

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 cDNA sequence

<400> 39 60 atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 120 atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 180 240 ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 300 gcctgcttcg tcctggtcct cacgcagage tccatcttca gtctcctggc catcgccatt gaccgctaca ttgccatccg catcccgctc cggtacaatg gcttggtgac cgggacgagg 360 getaagggca tcattgccat etgetgggtg etgtegtttg ccateggcet gacteccatg 420 ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg 480 540 gagggccaag tggcctdtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc 600 aacttetttg cetgtgtget ggtgeecetg etgeteatge tgggtgteta tttgeggate tteetggegg egegaegaea getgaageag atggagagee agtgttgtee ggggtgttgt 660 gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg 720 780 ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc ' gactgcagec acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840 teggttgtga atecetteat etaegeetae egtateegeg agtteegeea gaeetteege 900 960 aagatcatte geageeacgt eetgaggeag caagaacett teaaggeage tggeaceagt 1020 gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggt gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctqgtcga gctggacggc 1080

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gacgtaaacg	gccacaggtt	cagcgtgtcc	ggcgagggcg	agggcgatgc	cacctacggc	1140
aagctgaccc	tgaagttcat	ctgcaccacc	ggcaagctgc	ccgtgccctg	gcccaccctc	1200
gtgaccaccc	tgacctgggg	cgtgcagtgc	ttcagccgct	accccgacca	catgaagcag	1260
cacgacttct	tcaagtccgc	catgcccgaa	ggctacgtcc	aggagcgtac	catcttcttc	1320
aaggacgacg	gcaactacaa	gacccgcgcc	gaggtgaagt	tcgagggcga	caccctggtg	1380
aaccgcatcg	agctgaaggg	catcgacttc	aaggaggacg	gcaacatcct	ggggcacaag	1440
ctggagtaca	actacatcag	ccacaacgtc	tatatcaccg	ccgacaagca	gaagaacggc	1500
atcaaggccc	acttcaagat	ccgccacaac	atcgaggacg	gcagcgtgca	gctcgccgac	1560
cactaccagc	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	1620
ctgagcaccc	agtccgccct	gagcaaagac	cccaacgaga	agcgcgatca	catggtcctg	1680
ctggagttcg	tgaccgccgc	cgggatcact	ctcggcatgg	acgagctgta	caagtaa	1737

<210> 40

<211> 578

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 amino acid sequence

<400> 40

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile 70 75 80

·Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr 100 105 110

Asn	Gly	Leu 115	Val	Thr	Gly	Thr	Arg 120	Ala	Lys	Gly	Ile	Ile 125	Ala	Ile	Cys
Trp	Val 130	Leu	Ser	Phe	Ala	Ile 135	Gly	Leu	Thr	Pro	Met 140	Leu	Gly	Trp	Asn
Asn 145	Cys	Gly	Gln	Pro	Lys 150	Glu	Gly	Lys	Asn	His 155	Ser	Gln	Gly	Cys	Gly 160
Glu	Gly	Gln	Val	Ala 165	Cys	Leu	Phe	Glu	Asp 170	Val	Val	Pro	Met	Asn 175	Tyr
Met	Val	Tyr	Phe 180	Asn	Phe	Phe	Ala	Cys 185	Val	Leu	Val	Pro	Leu 190	Leu	Leu
Met	Leu	Gly 195	Val	Tyr	Leu	Arg	Ile 200	Phe	Leu	Ala	Ala	Arg 205	Arg	Gln	Leu
Lys	Gln 210	Met	Glu	Ser	Gln	Cys 215	Cys	Pro	Gly	Cys	Cys 220	Ala	Arg	Ser	Thr
Leu 225	Gln	Lys	Glu	Val	His 230	Ala	Ala	Lys	Ser	Leu 235	Ala	Ile	Ile	Val	Gly 240
Leu	Phe	Ala	Leu	Cys 245	Trp	Leu	Ь́ь	Leu	His 250	Ile	Ile	Asn	Суз	Phe 255	Thr
Phe	Phe	Суз	Pro 260	Asp	Cys	Ser	His	Ala 265	Pro	Leu	Trp	Leu	Met 270	Tyr	Leu
Ala	Ile	Val 275	Leu	Ser	His	Thr	Asn 280	Ser	Val	Val	Asn	Pro 285	Phe	Ile	Tyr
Ala	Tyr 290	_	Ile	Arg	Glu	Phe 295	_	Gln	Thr	Phe	Arg 300		Ile	Ile	Arg
Ser 305		Val	Leu	Arg	Gln 310	Gln	Glu	Pro	Phe	Lys 315	Ala	Ala	Gly	Thr	Ser 320
Ala	Arg	Val	Leu	Ala 325		His	Gly	Ser	Asp 330		Glu	Gln	Val	Ser 335	Leu
Arg	Leu	Asn	Gly	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	.Val

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350 345 340 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser 360 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu ` 375 380 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu 395 Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr 420 Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr 440 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu 455 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 475 470 Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys 490 485 Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu 505 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 520 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu

55/66

Tyr Lys

<210> 41 <211> 1686 DNA <213> artificial sequence <220> <223> A2A-FlashPG-CFP-C33 cDNA sequence <400> 41 atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 60 atectgggea atgtgctggt gtgctgggec gtgtggetca acagcaacet gcagaacgte 120 180 accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240 gcctgcttcg tcctggtcct cacgcagage tccatcttca gtctcctggc catcgccatt 300 360 gaccgctaca ttgccatccg catcccgctc cggtacaatg gcttggtgac cgggacgagg gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg 420 ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg 480 gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc 540 600 aacttetttg cetgtgtget ggtgeecetg etgeteatge tgggtgteta tttgeggate ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt 660 gcacggtcca cactgcagaa ggaggtccat gctgccaaqt cactggccat cattgtgggg 720 ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc 780 gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840 900 teggttgtga atcecttcat etacgeetae egtateegeg agtteegeea gacetteege aagatcatte geageeaegt eetgaggeag caagaaeett teaaggeage tggeaeeagt 960 gcccgggtcg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag 1020 1080 ctggacggcg acgtaaacgg ccacaggttc agcgtgtccg gcgagggcga gggcgatgcc acctacggca agetgaccet gaagtteate tgeaccaceg geaagetgee egtgeeetgg 1140 1200 cccaccctcg tgaccaccct gacctggggc gtgcagtgct tcagccgcta ccccgaccac atgaagcagc acgacttett caagteegee atgeeeqaag getaegteea ggagegtaee 1260 atcttcttca aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac 1320 accetggtga accgcatega getgaaggge ategaettea aggaggaegg caacateetg 1380

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gggcacaagc tggagtacaa	ctacatcagc	cacaacgtct	atatcaccgc	cgacaagcag	1440
aagaacggca tcaaggccca	cttcaagatc	cgccacaaca	tcgaggacgg	cagcgtgcag	1500
ctcgccgacc actaccagca	gaacaccccc	atcggcgacg	gccccgtgct	gctgcccgac	1560
aaccactacc tgagcaccca	gtccgccctg	agcaaagacc	ccaacgagaa	gcgcgatcac	1620
atggtcctgc tggagttcgt	gaccgccgcc	gggatcactc	tcggcatgga	cgagctgtac	1680
aagtaa					1686

<210> 42

<211> 561

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 amino acid sequence

<400> 42

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr 100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn 130 . 135 140

Asn 145	Cys	Gly	Gln	Pro	Lys 150	Glu	Gly	Lys	Asn	His 155	Ser	Gln	Gly	Суз	Gly 160
Glu	Gly	Gln	Val	Ala 165	Суз	Leu	Phe	Glu	Asp 170	Val	Val	Pro	Met	Asn 175	Tyr
Met	.Val	Туг	Phe 180	Asn	Phe	Phe	Ala	Cys 185	Val	Leu	Val	Pro	Leu 190	Leu	Leu
Met	Leu	Gly 195	Val	Tyr	Leu	Arg	Ile 200	Phe	Leu	Ala	Ala	Arg 205	Arg	Gln	Leu
Lys	Gln 210	Met	Glu	Ser	Gln	Cys 215	Суз	Pro	Gly	Суз	Cys 220	Ala	Arg	Ser	Thr
Leu 225	Gln	Lys	Glu	Val	His 230	Ala	Ala	Lys	Ser	Leu 235	Ala	Ile	Ile	Val	Gly 240
Leu	Phe	Ala	Leu	Cys 245	Trp	Leu	Pro	Leu	His 250	Ile	Ile	Asn	Суз	Phe 255	Thr
Phe	Phe	Суз	Pro 260	Asp	Суз	Ser	His	Ala 265	Pro	Leu	Trp	Leu	Met 270	Tyr	Leu
Ala	Ile	Val 275	Leu	Ser	His	Thr	Asn 280	Ser	Val	Val	Asn	Pro 285	Phe	Ile	Tyr
Ala	Tyr 290	Arg	Ile	Arg	Glu	Phe 295	Arg	Gln	Thr	Phe	Arg 300	Lys	Ile	Ile	Arg
Ser 305	His	Val	Leu	Arg	Gln 310	Gln	·Glu	Pro	Phe	Lys 315	Ala	Ala	Gly	Thr	Ser 320
Ala	Arg	Val	Val	Ser 325	_	Gly	Glu	Glu	Leu 330		Thr	Gly	Val ·	Val 335	Pro
Ile	Leu	Val	Glu 340	Leu	Asp	Gly	Asp	Val 345		Gly	His	Arg	Phe 350	Ser	Val
Ser	Gly	Glu 355		Glu	Gly	Asp	Ala 360		Tyr	Gly	Lys	Leu 365	Thr	Leu	Lys
Phe	Ile 370		Thr	Thr	Gly	Lys 375		Pro	Val	Pro	Trp 380		Thr	Leu	Val

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Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His 385 390 395 400 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 405 410 415 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 420 425 430 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 435 440 445 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 450 455 Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp 485 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 505 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser 520 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 535 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

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<223> A2A-CFP-ModelPG-C49 cDNA sequence

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Leu	Asn	Ser 35	Asn	Leu	Gln	Asn	Val 40	Thr	Asn	Tyr	Phe	Val 45	Val	Ser	Leu
Ala	Ala 50	Ala	Asp	Ile	Ala	Val 55	Gly	Val	Leu	Ala	Ile 60	Pro	Phe	Ala	Ile
Thr 65	Ile	Ser	Thr	Gly	Phe 70	Суз	Ala	Ala	Cys	His 75	Gly	Cys	Leu	Phe	Ile 80
Ala	Суз	Phe	Val	Leu 85	Val	Leu	Thr	Gln	Ser 90	Ser	Ile	Phe	Ser	Leu 95	Leu
Ala	Ile	e Ala	Ile 100	Asp	Arg	Tyr	Ile	Ala 105	Ile	Arg	Ile	Pro	Leu 110	Arg	Tyr
Asn	Gl	, Leu 115		Thr	Gly	Thr	Arg 120	Ala	Lys	Gly	Ile	Ile 125	Ala	Ile	Cys
Trp	Va]	L Leu)	Ser	Phe	Ala	Ile 135	Gly	Leu	Thr	Pro	Met 140	Leu	Gly	Trp	Asn
Asn 145	Сys	з Gly	Gln	Pro	Lys 150	Glu	Gly	Lys	Asn	His 155	Ser	Gln	Gly	Суз	Gly 160
Glu	Gl	y Gln	val	Ala 165		Leu	Phe	Glu	Asp 170		Val	Pro	Met	Asn 175	Tyr
Met	۷a	l Tyr	Phe 180		Phe	Phe	Ala	Cys 185		Leu	Val	Pro	Leu 190		Leu

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Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr 215 Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly 230 235 Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr 250 Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu 265 Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu 325 330 Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val 340 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser 355 360 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu 375 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu 385 Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp 405 His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr 420 · 425

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Val Glu Glu Arg Thr Ile Phe Phe Lys Asp Gly Asn Tyr Lys Thr 440 435 445 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu 450 455 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 470 465 Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys 485 495 Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu 500 505 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 515 520 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln 530 535 540 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 545 550 555 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 565 570 575 Tyr Lys Ala Glu Ala Ala Ala Arg Glu Ala Cys Cys Pro Gly Cys Cys 585 Ala Arg Ala 595 <210> 45 <211> 1737 <212> DNA <213> artificial sequence <220> <223> A2A-CFP-C49 cDNA sequence <400> 45 60 atgeceatea tgggeteete ggtgtacate aeggtggage tggecattge tgtgetggee atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc 120 180 accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc

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gctaagggca	tcattgccat	ctgctgggtg	ctgtcgtttg	ccatcggcct	gactcccatg	420
ctaggttgga	acaactgcgg	tcagccaaag	gagggcaaga	accactccca	gggctgcggg	480
gagggccaag	tggcctgtct	ctttgaggat	gtggtcccca	tgaactacat	ggtgtacttc	540
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cactaccagc	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	1620
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<210> 46 <211> 578 <212> PRT <213> artificial sequence

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<220> <223> A2A-CFP-C49 amino acid sequence <400> 46 Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp 30 . Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile 50 Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile 70. Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu 85 . Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr 100 Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys 115 120 125 Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn 130 135 Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr 170 Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu 185 Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr 210 215 220

Leu 225	Gln	Lys	Glu	Val	His 230	Ala	Ala	Lys	Ser	Leu 235	Ala	Ile	Ile	Val	Gly 240
Leu	Phe	Ala ·	Leu	Cys 245	Trp	Leu	Pro	Leu	His 250	Ile	Ile	Asn	Суз	Phe 255	Thr
Phe	Phe	Cys	Pro 260	Asp	Суз	Ser	His	Ala 265	Pro	Leu	Trp	Leu	Met 270	Tyr	Leu
Ala	Ile	Val 275	Leu	Ser	His	Thr	Asn 280	Ser	Val	Val	Asn	Pro 285	Phe	Ile	Tyr
Ala	Туг 290	Arg	Ile	Arg	Glu	Phe 295	Arg	Gln	Thr	Phe	Arg 300	Lys	Ile	Ile	Arg .
Ser 305	His	Val	Leu	Arg	Gln 310	Gln	Glu	Pro	Phe	Lys 315	Ala	Ala	Gly	Thr	Ser 320
Ala	Arg	Val	Leu	Ala 325	Ala	His	Gly	Ser	Asp 330	Gly	Glu	Gln	Val	Ser 335	Leu
Arg	Leu	Asn	Gly 340	Val	Ser	Lys	Gly	Glu 345	Glu	Leu	Phe	Thr	Gly 350	Val	Val
Pro	Ile	Leu 355	Val	Glu	Leu	Asp	Gly 360	Asp	Val	Asn	Gly	His 365	Arg	Phe	Ser
Val	Ser 370	Gly	Glu	Gly	Glu	Gly 375	Asp	Ala	Thr	Tyr	Gly 380	Lys	Leu	Thr	Leu
Lys 385	Phe	Ile	Суз	Thr	Thr 390	Gly	Lys	Leu	Pro	Val 395	Pro	Trp	Pro	Thr	Leu 400
Val	Thr	Thr	Leu	Thr 405	_	Gly	Val	Gln	Cys 410	Phe	Ser	Arg	Tyr	Pro 415	Asp
His	Met	Lys	Gln 420		Asp	Phe	Phe	Lys 425	Ser	Ala	Met	Pro	Glu 430	_	Tyr
Val	Gln	Glu 435	_	Thr	Ile	Phe	Phe 440	-	Asp	Asp	Gly	Asn 445	. –	Lys	Thr
Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	. Val	. Asn	Arg	, Ile	Glu

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450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485
490
495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu 500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln 530 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 565 570 575

Tyr Lys

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